RAW SEQUENCE LISTING PATENT APPLICATION US/09/292,411

DATE: 11/28/2000 TIME: 02:39:54

INPUT SET: S36148.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQUENCE LISTING
2	(1)	
3 4	(1)	General Information:
5 6 7 8		(i) APPLICANT: Payne, David Lonsdale, John Milner, Peter Pearson, Stewart
9 10 11 12		(ii) TITLE OF INVENTION: FAB I
13 14		(iii) NUMBER OF SEQUENCES: 2
15		(iv) CORRESPONDENCE ADDRESS:
16		(A) ADDRESSEE: Dechert Price & Rhoads
17		(B) STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
18		(C) CITY: Philadelphia
19		(D) STATE: PA
20		(E) COUNTRY: US
21		(F) ZIP: 19103
22		(-)
23		(v) COMPUTER READABLE FORM:
24		(A) MEDIUM TYPE: Diskette
25		(B) COMPUTER: IBM Compatible
26		(C) OPERATING SYSTEM: Windows 95
27		(D) SOFTWARE: FastSEO for Windows Version 2.0b
28		(2) 202 1111 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
29	,	(vi) CURRENT APPLICATION DATA:
30		(A) APPLICATION NUMBER: 09/292,411
31		(B) FILING DATE:
32		(C) CLASSIFICATION:
33		(0) 0220222011
34		(vii) PRIOR APPLICATION DATA:
35		(A) APPLICATION NUMBER: 08/790,043
36		(B) FILING DATE:
37		(5, 112110 2112)
38		
39		
40		(viii) ATTORNEY/AGENT INFORMATION:
41		(A) NAME: Falk, Stephen T
42		(B) REGISTRATION NUMBER: 36,795
43		(C) REFERENCE/DOCKET NUMBER: GM50005
44		(C) REFERENCE/ DOCKET HORDER. GROUDS
45		(ix) TELECOMMUNICATION INFORMATION:
46		(A) TELEPHONE: 215-994-2488

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```
(B) TELEFAX: 215-994-2222
47
             (C) TELEX:
48
49
50
           (2) INFORMATION FOR SEQ ID NO:1:
51
52
           (i) SEQUENCE CHARACTERISTICS:
53
             (A) LENGTH: 771 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
57
             (D) TOPOLOGY: linear
58
59
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61
     ATGTTAAATC TTGAAAACAA AACATATGTC ATCATGGGAA TCGCTAATAA GCGTAGTATT
                                                                           60
62
     GCTTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA AATTAGTATT TACTTACCGT
63
                                                                           120
     AAAGAACGTA GCCGTAAAGA GCTTGAAAAA TTATTAGAAC AATTAAATCA ACCAGAAGCG
64
                                                                           180
     CACTTATATC AAATTGATGT TCAAAGCGAT GAAGAGGTTA TTAATGGTTT TGAGCAAATT
                                                                           240
     GGTAAAGATG TTGGCAATAT TGATGGTGTA TATCATTCAA TCGCATTTGC TAATATGGAA
66
67
     GACTTACGCG GACGCTTTTC TGAAACTTCA CGTGAAGGCT TCTTGTTAGC TCAAGACATT
     AGTTCTTACT CATTAACAAT TGTGGCTCAT GAAGCTAAAA AATTAATGCC AGAAGGTGGT
68
                                                                           420
     AGCATTGTTG CAACAACATA TTTAGGTGGC GAATTCGCAG TTCAAAATTA TAATGTGATG
                                                                           480
69
   GGTGTTGCTA AAGCGAGCTT AGAAGCAAAT GTTAAATATT TAGCATTAGA CTTAGGTCCT
                                                                          540
70
71 GATAATATTC GCGTTAATGC AATTTCAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT
                                                                           600
72 GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT AAAACGTAAC
                                                                          660
73 GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTRT TAAGTGACTT ATCAAGTGGC
                                                                          720
     GTTACAGGTG AAAATATTCA TGTAGATAGC GGATTCCACG CAATTAAATA A
                                                                          771
74
75
               (2) INFORMATION FOR SEQ ID NO:2:
76
77
78
           (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 256 amino acids
79
             (B) TYPE: amino acid
80
             (C) STRANDEDNESS: single
81
82
             (D) TOPOLOGY: linear
83
84
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
85
86
     Met Leu Asn Leu Glu Asn Lys Thr Tyr Val Ile Met Gly Ile Ala Asn
87
88
                                         10
     Lys Arg Ser Ile Ala Phe Gly Val Ala Lys Val Leu Asp Gln Leu Gly
89
90
91
     Ala Lys Leu Val Phe Thr Tyr Arg Lys Glu Arg Ser Arg Lys Glu Leu
                                 40
     Glu Lys Leu Leu Glu Gln Leu Asn Gln Pro Glu Ala His Leu Tyr Gln
93
94
                             55
     Ile Asp Val Gln Ser Asp Glu Glu Val Ile Asn Gly Phe Glu Gln Ile
95
96
                        70
                                             75
97
     Gly Lys Asp Val Gly Asn Ile Asp Gly Val Tyr His Ser Ile Ala Phe
98
                                         90
                     85
     Ala Asn Met Glu Asp Leu Arg Gly Arg Phe Ser Glu Thr Ser Arg Glu
```

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100				100					105					110		
101	Gly	Phe	Leu	Leu	Ala	${\tt Gln}$	Asp	Ile	Ser	Ser	Tyr	Ser	Leu	Thr	Ile	Val
102			115					120					125			
103	Ala	His	Glu	Ala	Lys	Lys	Leu	Met	Pro	Glu	Gly	Gly	Ser	Ile	Val	Ala
104		130					135					140				
105	Thr	$\overline{\mathtt{n}}\mathtt{n}\mathtt{r}$	īyr	Leu	Gly	Gly	Glu	Phe	Ala	Val	Gln	Asn	Tyr	Asn	Val	Met
106	145					150					155					160
107	Gly	Val	Ala	Lys	Ala	Ser	Leu	Glu	Ala	Asn	Val	Lys	Tyr	Leu	Ala	Leu
108					165					170					175	
109	Asp	Leu	Gly	Pro	Asp	Asn	Ile	Arg	Val	Asn	Ala	Ile	Ser	Ala	Gly	Pro
110				180					185					190		
111	Ile	Arg	Thr	Leu	Ser	Ala	Lys	Gly	Val	Gly	Gly	Phe	Asn	Thr	Ile	Leu
112			195					200					205			
113	Lys	Glu	Ile	Glu	Glu	Arg	Ala	Pro	Leu	Lys	Arg	Asn	Val	Asp	Gln	Val
114		210					215					220				
115	Glu	Val	Gly	Lys	Thr	Ala	Ala	Tyr	Leu	Leu	Ser	Asp	Leu	Ser	Ser	Gly
116	225		_			230					235					240
117	Val	Thr	Gly	Glu	Asn	Ile	His	Val	Asp	Ser	Gly	Phe	His	Ala	Ile	Lys
118			_		245					250					255	
119		•														

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/292,411

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Line Error

Original Text

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/09/292,411

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< < THERE ARE NO ITEMS MISSING >>

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/09/292,411

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Line

Original Text

Corrected Text